



**Title: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
IMPAIRED GLUCOSE TOLERANCE CONDITIONS**

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Comparison of the human AKT protein sequence to the cosmid sequence C12D8, located in the genetic interval where sup(mg144) maps. Numbering in the AKT protein sequence by amino acid residues, and in the cosmid sequence by nucleotide position.

**Score = 450 (207.4 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165
Identities = 79/121 (65%), Positives = 97/121 (80%), Frame = +1**

**SEQ ID No: 87 Query: 319 EVLEDNDYGRAVDWWGLGVVMYEMMCGRLPFYQNQDHEKLFELILMEEIRFPRTLGPEAKS 378
SEQ ID No: 325 +VL+D+DYGR VDWG+GVVMYEMMCGRLPFY++DH KLFELI+ ++RFP L EA++
SEQ ID No: 88 Sbjct: 33685 QVLDDHDYGRGCVDDWVGVGVVMYEMMCGRLPFYSKDHNLKLFELIMAGDLRFP SKLSQEART 33864**

**Query: 379 LLSGGLLKDPTQRLGGGSEDAKEIMQHRRFPANIVWQDVYEKKLSPPFKPQVTSETDTRYFD 439
LL+GLL KDPTQRLGGG EDA EI + FF + W+ Y K++ PP+KP V SETDT YFD
Sbjct: 33865 LLTGLLVKDPTQRLGGGPEDALEICRADFPRTVDWEATYRKEIEPPYKPNVQSETDTSYFD 34047**

**Score = 256 (118.0 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165
Identities = 48/66 (72%), Positives = 59/66 (89%), Frame = +1**

**SEQ ID No: 89 Query: 146 TMNEFEYLKLLGKGTGKVLVKEKATGRYYAMKILKKEVIVAKDEVARTLTERVLQNS 205
SEQ ID No: 326 TM +F++LK+LGKGTGKVLV KEK T + YA+KILKK+VI+A++EVARTLTERVLQ
SEQ ID No: 90 Sbjct: 32314 TMEDPDFLKVLGKGTGKVLCKEKTQKLYAIKILKKDVIAREEEVAHTLTERVLQRC 32493**

**Query: 206 RHPFLT 211
+HPFLT
Sbjct: 32494 KHPFLT 32511**

**Score = 190 (87.6 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165
Identities = 36/45 (80%), Positives = 37/45 (82%), Frame = +2**

**SEQ ID No: 91 Query: 276 KLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPEV 320
KLENL+LDKDGHIKI DFGLCKE I G TFCGTPEYLAPEV
SEQ ID No: 99 Sbjct: 33509 KLENLLDKDGHIKIADFGLCKEISPGDKTSTFCGTPEYLAPEV 33643**

**Score = 188 (86.7 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165
Identities = 37/57 (64%), Positives = 42/57 (73%), Frame = +3**

**SEQ ID No: 93 Query: 209 FLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAEVSAALYH 265
SEQ ID No: 100 + LKYSFQ LCFVM++ANGGELF H+ + FSE RARFYGAEV AL YLH
SEQ ID No: 94 Sbjct: 32667 YFQELKYSFQEQHYLCFVMQFANGGELFTHVRKCGTFSEPRARFYGAEVLAALYH 32837**

**Score = 166 (76.5 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165
Identities = 29/59 (49%), Positives = 42/59 (71%), Frame = +1**

**SEQ ID No: 95 Query: 53 NNFSVAQCQLMKTERPRPNNTFIIRCLQWTTVIERTFHVTPEEREEWATAIQTVDGLK 111
+ F++ Q M E+PRPN F++RCLQWTTVIERTF+ E+ E R+ W AI++++ K
SEQ ID No: 101 Sbjct: 31846 STFAIFYFQTMLFEKPRPNMFVRCLQWTTVIERTFYAESAEVRQRWIHAIESISKYK 32022**

**Score = 134 (61.8 bits), Expect = 5.2e-167, Sum P(8) = 5.2e-167
Identities = 24/33 (72%), Positives = 30/33 (90%), Frame = +3**

**SEQ ID No: 97 Query: 210 LTALKYSFQTHDRLCFVMEYANGGELFFHLSRE 242
SEQ ID No: 102 L LKYSFQT+DRLCFVME+A GG+L++HL+RE
SEQ ID No: 98 Sbjct: 33156 LQELKYSFQTNDRLCFVMEFAIGGDLYYHNLRE 33254**

Fig. 25